

FIGURE 1A

1 CGGGCCTGAGACTGGGGTGGTGGGACCTAAGAGAATCCTGAGCTGGAGGGCCCCCGACAG
 61 CTGCTCTCGGGAGCCGCCTCCCGACACCCGAGCCCCGCGGCGCTCCCGCTCCCGGCTC
 121 CCGGCTCCTGGCTCCCTCCGCCTCCCCCGCCCCCTCGCCCCGCGCGCCGAAGAGGCCCCGCT
 181 CCCGGGTCGGACGCCTGGGTCTGCCGGGAAGAGCGATGAGAGGTGTCTGAAGGTGGCTAT
 241 TCACTGAGCGATGGGGTTGGACTTGAAGGAATGCCAAGAGATGCTGCCCCCACCCTTA

 1 M G P E A L S S L L L L L L L
 301 GGCCCCGAGGGATCAGGAGCTATGGGACCAGAGGCCCTGTCATCTTTACTGCTGCTGCTCT
 15 V A S G D A D M K G H F D P A K C R Y A
 361 TGGTGGCAAGTGGAGATGCTGACATGAAGGGACATTTTGATCCTGCCAAGTGCCGCTATG
 35 L G M Q D R T I P D S D I S A S S S W S
 421 CCCTGGGCATGCAGGACCGGACCATCCAGACAGTGACATCTCTGCTTCCAGCTCCTGGT
 55 D S T A A R H S R L E S S D G D G A W C
 481 CAGATTCCACTGCCGCCCGCCACAGCAGGTGGAGAGCAGTGACGGGGATGGGGCCTGGT
 75 P A G S V F P K E E E Y L Q V D L Q R L
 541 GCCCCGAGGGTGGGTGTTTCCCAAGGAGGAGGAGTACTTGCAGGTGGATCTACAACGAC
 95 H L V A L V G T Q G R H A G G L G K E F
 601 TCACCTGGTGGCTCTGGTGGGCACCCAGGACCGCATGCCGGGGGCTGGGCAAGGAGT
 115 S R S Y R L R Y S R D G R R W M G W K D
 661 TCCTCCCGGAGCTACCGGCTGCGTTACTCCCGGATGGTCCCGCTGGATGGGCTGGAAGG
 135 R W G Q E V I S G N E D P E G V V L K D
 721 ACCGCTGGGGTCAAGGAGGTGATCTCAGGCAATGAGGACCCTGAGGGAGTGGTGTGAAGG
 155 L G P P M V A R L V R F Y P R A D R V M
 781 ACCTTGGGCCCCCATGGTTGCCGACTGGTTGCTTCTACCCCCGGGCTGACCGGGTCA
 175 S V C L R V E L Y G C L W R D G L L S Y
 841 TGAGTGCTGTCTGCGGGTAGAGCTCTATGGCTGCCTCTGGAGGGATGGACTCCTGTCTT
 195 T A P V G Q T M Y L S E A V Y L N D S T
 901 ACACCGCCCCCTGTGGGGCAGACAATGTATTATCTGAGGCCGTGTACCTCAACGACTCCA
 215 Y D G H T V G G L Q Y G G L G Q L A D G
 961 CCTATGACGGACATACCGTGGGCGGACTGCAGTATGGGGGTCTGGGCCAGCTGGCAGATG
 235 V V G L D D F R K S Q E L R V W P G Y D
 1021 GTGTGGTGGGGCTGGATGACTTTAGGAAGAGTCAGGAGCTGCGGGTCTGGCCAGGCTATG
 255 Y V G W S N H S F S S G Y V E M E F E F
 1081 ACTATGTGGGATGGAGCAACCACAGCTTCTCCAGTGGCTATGTGGAGATGGAGTTTGTAGT
 275 D R L R A F Q A M Q V H C N N M H T L G
 1141 TTGACCGGCTGAGGGCCTTCCAGGCTATGCAGGTCCACTGTAAACAACATGCACACGCTGG
 295 A R L P G G V E C R F R R G P A M A W E
 1201 GAGCCCGTCTGCCGCGGGTGAATGTGCTTCCGGCGTGGCCCTGCCATGGCCTGGG
 315 G E P M R H N L G G N L G D P R A R A V
 1261 AGGGGGAGCCCATGCGCCACAACCTAGGGGGCAACCTGGGGGACCCAGAGCCCGGGCTG
 335 S V P L G G R V A R F L Q C R F L F A G
 1321 TCTCAGTGCCCCCTGGCGGCGGTGTGGCTCGCTTCTGTCAGTGCCGCTTCTCTTTGCGG
 355 P W L L F S E I S F I S D V V N N S S P
 1381 GGCCCTGGTTACTCTTCAGCGAAATCTCCTTCATCTCTGATGTGGTGAACAATTCCTCTC

FIGURE 1B

375 A L G G T F P P A P W W P P G P P P T N
 1441 CGGCACTGGGAGGCACCTTCCCCCAGCCCCCTGGTGGCCGCCTGGCCCCACCTCCACCA
 395 F S S L E L E P R G Q Q P V A K A E G S
 1501 ACTTCAGCAGCTTGGAGCTGGAGCCCAGAGGCCAGCAGCCGTGGCCAAGGCCGAGGGGA
 415 P T A I L I G C L V A I I L L L L L I I
 1561 GCCCGACCGCCATCTCATCGGCTGCCTGGTGGCCATCATCTGCTCCTGCTGCTCATCA
 435 A L M L W R L H W R R L L S K A E R R V
 1621 TTGCCCTCATGCTCTGGCGGCTGCACTGGCGCAGGCTCCTCAGCAAGGCTGAACGGAGGG
 455 L E E E L T V H L S V P G D T I L I N N
 1681 TGTTGGAAGAGGAGCTGACGGTTACCTCTCTGTCCCTGGGGACACTATCCTCATCAACA
 475 R P G P R E P P P Y Q E P R P R G N P P
 1741 ACCGCCAGGTCTAGAGAGCCACCCCGTACCAGGAGCCCCGGCCTCGTGGAATCCGC
 495 H S A P C V P N G S A L L L S N P A Y R
 1801 CCCACTCCGCTCCCTGTGTCCCCAATGGCTCTGCGTTGCTGCTCTCCAATCCAGCCTACC
 515 L L L A T Y A R P P R G P G P P T P A W
 1861 GCCTCCTTCTGGCCACTTACGCCCCGCCCCCTCGAGGCCCGGGCCCCCCCCACACCCGCT
 535 A K P T N T Q A Y S G D Y M E P E K P G
 1921 GGGCCAAACCCACCAACACCCAGGCCACAGTGGGGACTATATGGAGCCTGAGAAGCCAG
 555 A P L L P P P P Q N S V P H Y A E A D I
 1981 GCGCCCCGCTTCTGCCCCCACCTCCCCAGAACAGCGTCCCCCATATGCGGAGGCTGACA
 575 V T L Q G V T G G N T Y A V P A L P P G
 2041 TTGTTACCCTGCAGGGCGTCACCGGGGCAACACCTATGCTGTGCCTGCACTGCCCCCAG
 595 A V G D G P P R V D F P R S R L R F K E
 2101 GGGCAGTCGGGGATGGGCCCCCAGAGTGGATTTCCTCGATCTCGACTCCGCTTCAAGG
 615 K L G E G O F G E V H L C E V D S P Q D
 2161 AGAAGCTTGGCGAGGGCCAGTTGGGGAGGTGCACCTGTGTGAGGTGCACAGCCCTCAAG
 635 L V S L D F P L N V R K G H P L L V A V
 2221 ATCTGGTCAGTCTTGATTTCCTTAAATGTGCGTAAGGGACACCCTTTGCTGGTAGCTG
 655 K I L R P D A T K N A S F S L F S R N D
 2281 TCAAGATCTTACGGCCAGATGCCACCAAGAATGCCAGCTTCTCCTTGTCTCCAGGAATG
 675 F L K E V K I M S R L K D P N I I R L L
 2341 ATTTCTGAAAGAGGTGAAGATCATGTGAGGCTCAAGGACCCCAACATCATTCGGCTGC
 695 G V C V Q D D P L C M I T D Y M E N G D
 2401 TGGGCGTGTGTGTGAGGACGACCCCCCTCTGCATGATTACTGACTACATGGAGAACGGCG
 715 L N Q F L S A H Q L E D K A A E G A P G
 2461 ACCTCAACCAGTTCTCAGTGCCACCAGCTGGAGGACAAGGCAGCCGAGGGGGCCCCCTG
 735 D G Q A A Q G P T I S Y P M L L H V A A
 2521 GGGACGGGCAGGCTGCGCAGGGGGCCACCATCAGCTACCCAATGCTGCTGTCATGTGGCAG
 755 Q I A S G M R Y L A T L N F V H R D L A
 2581 CCCAGATCGCTCCGGCATGCGCTATCTGGCCACACTCAACTTTGTACATCGGGACCTGG
 775 T R N C L V G E N F T I K I A D F G M S
 2641 CCACGCGGAACGCCTAGTTGGGGAAAATTCACCATCAAAATCGCAGACTTTGGCATGA

FIGURE 1C

795 R N L Y A G D Y Y R V Q G R A V L P I R
2701 GCCGGAACCTCTATGCTGGGGACTATTACCGTGTGCAGGGCCGGGCAGTGCTGCCCCATCC
815 W M A W E C I L M G K F T T A S D V W A
2761 GCTGGATGGCCTGGGAGTGCATCCTCATGGGGAAGTTCACGACTGCGAGTGACGTGTGGG
835 F G V T L W E V L M L C R A Q P F G Q L
2821 CCTTTGGTGTGACCCTGTGGGAGGTGCTGATGCTCTGTAGGGCCCCAGCCCTTTGGGCAGC
855 T D E Q V I E N A G E F F R D Q G R Q V
2881 TCACCGACGAGCAGGTTCATCGAGAACGCGGGGAGTTCTTCCGGGACCAGGGCCGGCAGG
875 Y L S R P P A C P Q G L Y E L M L R C W
2941 TGTACCTGTCCCGGCCGCTGCTGCCCGCAGGGCCTATATGAGCTGATGCTTCGGTGCT
895 S R E S E Q R P P F S Q L H R F L A E D
3001 GGAGCCGGGAGTCTGAGCAGCGACCACCTTTTCCCAGCTGCATCGGTTCCTGGCAGAGG
915 A L N T V
3061 ATGCACTCAACACGGTGTGAATCACACATCCAGCTGCCCCCTCCCTCAGGGAGTGATCCAG
3121 GGAAGCCAGTGACACTAAAACAAGAGGACACAATGGCACCTCTGCCCTTCCCCCTCCCGA
3181 CAGCCCATCACCTCTAATAGAGGCAGTGAGACTGCAGGTGGGCTGGGCCCCACCCAGGGAG
3241 CTGATGCCCTTCTCCCCCTTCTGGACACACTCTCATGTCCCCCTTCTGTCTTCTTCTTCC
3301 TAGAAGCCCCCTGTGCCCCACCCAGCTGGTCTGTGGATGGGATCCTCTCCACCTTCTCT
3361 AGCCATCCCTTGGGGGAAGGGTGGGGAGAAATATAGGATAGACACTGGACATGGCCCCATTG
3421 GAGCACCTGGGCCCCACTGGACAACACTGATTCTTGGAGAGGTGGCTGCGCCCCAGCTTC
3481 TCTCTCCCTGTACACACTGGACCCCACTGGCTGAGAATCTGGGGGTGAGGAGGACAAGA
3541 AGGAGAGGAAAATGTTTCTTGTGCTGCTCTGTACTTGTCTCAGCTTGGGCTTCTTC
3601 CTCCTCCATCACCTGAAACACTGGACCTGGGGGTAGCCCCGCCAGCCCTCAGTCACCC
3661 CCACTTCCCACTGTCAGTCTGTAGCTAGAACTTCTCTAAGCCTATACGTTTCTGTGGAG
3721 TAAATATTGGGATTGGGGGAAAGAGGGAGCAACGGCCCCATAGCCTTGGGGTTGGACATC
3781 TCTAGTGTAGCTGCCACATTGATTTTTCTATAATCACTTGGGGTTGTACATTTTTGGGG
3841 GGAGAGACACAGATTTTACACTAATATATGGACCTAGCTTGAGGCAATTTTAATCCCCT
3901 GCACTAGGCAGGTAATAATAAAGGTTGAGTTTTCCACAAAAAAAAAAAAAAAAACCGGAAT
3961 TC

FIGURE 2

MCK-10 Splice Variants

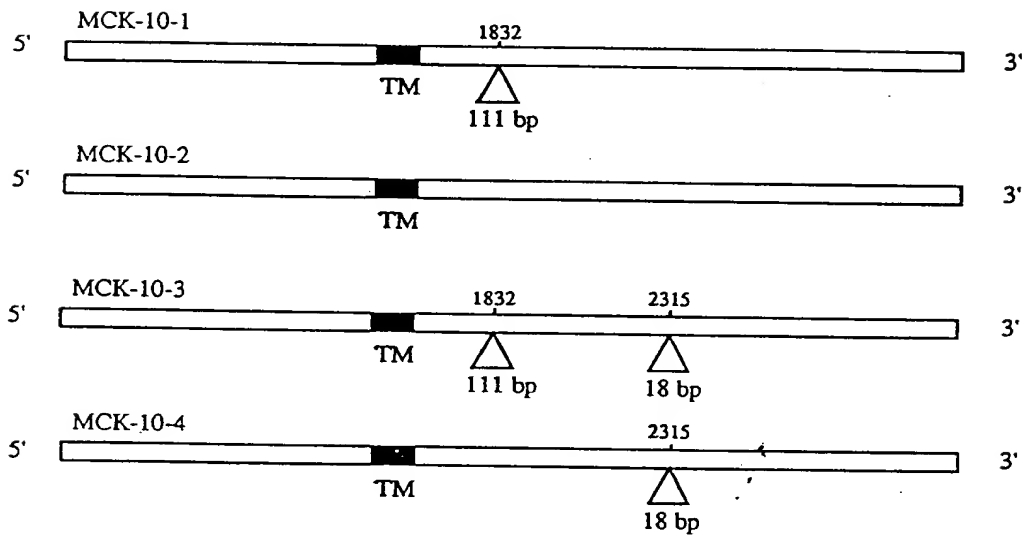


FIGURE 3A

2 gcacgagcggcagcagtgatgatctcttccatccctcccttctggttgcacttct 61
 cgtgctcgcctgctcaggtactagagaaggtaggagggaaaggactttcgagtgaaga
 b
 62 ttcttgcctcatcttggagactgtgcaatcccagattaactacaaacagagaagagctgg 121
 aaagaacgagtagaaccctcgacccgttagggctcaattgatgtttgtctcttctcgacc
 b
 122 tgatagctccagagctcagagaaggaggtctctttacaagaagctcggctctcaaagcc 181
 actatcgaggtctcgagctcttctccagagaaatgttctcagaccgagagtttcgg
 b
 182 tccatcaaggagacctaacaagtgcctggggttcagtgctctagaagttccaaggttt 241
 aggtagttccctctggatgttcaacggaccccaagtcacgagatcttcaaggttccaaa
 b
 242 gtggcttgaattattctaaagaagctgaaataattgaagagaagcagaggccagctgttt 301
 caccgaacttaataagatttctcgactttattaactctcttcgtctccggctcgacaaa
 b
 302 ttgaggatcctgctccacagagaatgctctgcacccgttgatactccagttccaacacca 361
 aactcctaggacgaggtgtctcttacgagacgtgggcaactatgaggtcaaggttgtggt
 b
 362 tctctcgagatgatcctgattccagaaatgctctgtgttctctgctgctgcttacc 421
 agaagactctactaggactaagggtcttacgagaaaccacgacaaggacgacgagatag
 b
 K I L I P R M L L V L F L L L P I -
 422 ttgagttctgcaaaagctcaggttaatccagctatatgccgctatcctctgggcatgtca 481
 aactcaagacgttttcgagtcgaattaggtcgatatacggcgataggagaccggtacagt
 b
 L S S A K A Q V N P A I C R Y P L G M S -
 482 ggaggccagattccagatgaggacatcacagcttccagtcagtggtcagagtcacacagct 541
 cctccggctcaagggtctactcctgtagtgtgaaggtcagtcacagctcaggtgtcga
 b
 G G Q I P D E D I T A S S Q W S E S T A -
 542 gccaaatatggaaggctggactcagaagaagggtatggagcctgggtgccctgagattcca 601
 cggtttataccttccgacctgagcttcttccctacctcggaccacgggactctaaggt
 b
 A K Y G R L D S E E G D G A W C P E I P -
 602 gtggaacctgatgacctgaaggagtttctgcagattgacttgcacacctccattttatc 661
 cacctggactactggacttccctcaaagacgtctaactgaacgtgtgggaggtaaaatag
 b
 V E P D D L K E F L Q I D L H T L H F I -
 662 actctggtggggaccaggggcccagcagaggtcatggcatcgagtttggcccatg 721
 tgagaccacccctgggtcccccgggtcgtctccagtcacctagctcaaacgggggtac
 b
 T L V G T Q G R R A G G H G I E F A P H -
 722 tacaagtcaattacagtcgggatggcactcgtggatctcttggcggaaccgtcatggg 781
 atgttctagttaattgtcagccctaccgtgagcgacctagagaaccgcttggcagttacc
 b
 Y K I H Y S R O G T R W I S W R N R H G -
 762 aaacgggtgctggatggaaatagtaaccctatgacatttccctaaaggacttggagccg 841
 ttgtccacgacctacctttatcatggggatactgtaaaaggatttctgaacctcggc

7683 31 (Sheet 5 of 30)

K Q V L O G N S N P Y D I F L K D L E P -

842 cccattgtlagccagatttctgcgggttcattccagtcaccgaccattccatgaattgtgtgt
gggtaacatcgggtctaaacaggccaagtaaggctcagtggtggtgaggtctctacacaca 901

b P I V A R F V R F I P V T D K S M N V C -

902 atgagagtgaggcttttacggCTGTGTCTGGCTAGATGGCTGGTGCTTACAATGCTCCA
tactctcacctcgaaatgcccGACACAGACCGATCTACCGAACACAGAATGTTACGAGGT 961

b H R V E L Y G C V H L D G L V S Y N A P -

962 GCTGGGCAGCAGTTTGTACTCCCTGGAGGTTCCATCATTTATCTGAATGATTCTGTCTAT
CGACCCGTCGTCAAACATGAGGGACCTCCAAGGTAGTAAATAGACTTACTAAGACAGATA 1021

b A G Q Q F V L P G G S I I Y L N D S V Y -

1022 GATGGAGCTGTTGGATACAGCATGACAGAAGGGCTAGGCCAATTGACCGATGGTGTGTCT
CTACCTCGACAACCTATGTCTGTCTCTCCGATCCGGTTAACTGGCTACCACACAGA 1081

b D G A V G Y S M T E G L G Q L T D G V S -

1082 GGCTGGACGATTTCAACCAGACCCATGAATACCAGCTGTGGCCCGGCTATGACTATGTG
CCGGACCTGCTAAAGTGGGTCGGGTACTTATGTGTCACACCGGGCCGATACTGATACAC 1141

b G L O D F T Q T H E Y H V H P G Y O Y V -

1142 GGCTGGCGGAACGAGAGTGCCACCAATGGCTACATTGAGATCATGTTTGAATTTGACCGC
CCGACCGCCTTGCTCTCACGGTGGTTACCGATGTAACCTAGTACAAACTTAACTGGCG 1201

b G W R N E S A T N G Y I E I M F E F D R -

1202 ATCAGGAATTTCACTACCATGAAGGTCCACTGCAACAACATGTTTGCTAAAGGTGTGAAG
TAGTCCTTAAAGTGATGGTACTTCCAGGTGACGTTGTTGTACAACGATTTCCACACTTC 1261

b I R K F T T M K V H C N N M F A K G V K -

1262 ATCTTTAAGGAGGTACAGTGCTACTTCCGCTCTGAAGCCAGTGAGTGGGTACCTAATGCC
TAGAAATTCCTCCATGTCCAGATGAAGGCGAGACTTCGGTCACTACCCATGGATTACGG 1321

b I F K E V Q C Y F R S E A S E H V P N A -

1322 ATTTCTTcccccttgccttgatgacgtcaaccaccagtgctcggtttgtcagcgtgcct
TAAAGGAAGgggggaacaggacctaactgcagttgggggtcacgagccadacagtgccacgga 1381

b I S F P L V L D D V N P S A R F V T V P -

1382 ctccaccaccgaatggccagtgccatcaagtgcaataccattttgcagatacctggatg
gaggtggtggtctaccgggtcaggtgagttcacagttatggttaaacgtctatggacctac 1441

b L H H R M A S A I K C Q Y H F A D T M H -

1442 atgttcagtgagatcaccttccaatcagatgctgcaatgtacaacaactctgaagccctg
tacaagtcactctagtggaaggttagtctacgacgttacatgttgttgagacttcgggac 1501

b H F S E I T F Q S D A A M Y K N S E A L -

1502 cccacctctcctatggcaccacaaacctatgatccaatgcttaagttgatgacagcaac
gggtggagaggataaccgtgggtgttgatactaggttacgaattcaactactgtcgttg 1561

b P T S P M A P T T Y D P M L K V D D S N -

1562 actcggatcctgattggtgcttgggtggccatcatctttatcctcctggccatcattgtc
tgagccttaggactaaccgacgaaccaccggtagtagaaataggaggaccggtagtaacag 1621

b T R I L I G C L V A I I F I L L A I I V -

1622 atcatcctctggaggcagttctggcagaaaatgctggagaaggcttctcggaggatgctg
tagtaggagacctccgtcaagaccgtcttttacgacctctccgaagagccctcctacgac 1681

b I I L W R Q F W Q K M L E K A S R R M L -

gatgatgaatgacagtcagcctttccctggccaagtgtatctagcatgttcaacaataac

1682
ctactactttactgtcagtcggaaggggcggttcactzagatcgtacaagtgtgtattg 1741

b
O D E M T V S L S L P S D S S M F K N N -
cgctccctcatcacctagtgzacaagggtcccaectcgacttacgacgcgcatctttcccccctt 1801
gcgaggagtagtggatcacttggttcccgaggttgagctgaatgctagcgtagaaaggggaa

1742
R S S S P S E Q G S N S T Y O R I F P L -
cgccctgactacCAGGAGCCATCCAGGCTGATACGAAAACCTCCAGAAATTTGCTCCAGGG 1861
gcgggactgatgTTCCTCGGTAGGTCCGACTATGCTTTTGAGGGTCTTAAACGAGGTCCC

b
R P D Y Q E P S R L I R K L P E F A P G -
GAGGAGGAGTCAGGCTGCAGCGGTGTGTGTAAGCCAGTCCAGCCCACTGCCCTGAGGGG 1921
CTCCTCCTCAGTCCGACGTCGCCACAACACTTCGGTCAGGTCCGGTCACCGGGACTCCCC

1862
E E E S G C S G V V K P V Q P S G P E G -
GTGCCCCACTATGCAGAGGCTGCATAGTGAACCTCCAAGGAGTGACAGGAGGCAACACA 1981
CACGGGGTGATACGTCTCCGACTGTATCACTTGGAGGTTCTCTACTGTCTCCGTGTGT

b
V P H Y A E A D I V N L Q G V T G G N T -
TACTCAGTGCCTGCCGTCAACATGGACCTGCTCTCAGGAAAAGATGTGGCTGTGGAGGAG 2041
ATGAGTCACGGACGGCAGTGGTACCTGGACGAGAGTCTCTTTCTACACCGACACCTCCTC

1982
Y S V P A V T M D L L S G K D V A V E E -
TTCCCCAGGAAACTCCTAACTTCAAAGAGAAGCTGGGAGAAGGACAGTTTGGGGAGGTT 2101
AAGGGGTCTCTTGAGGATTGAAAGTTTCTCTTCGACCTCTTCTCTCAAACDCTCCAA

b
F P R K L L T F K E K L G E G Q F G E V -
CATCTCTGTGAAGTGGAGGGAATGGAAAAATCAAGACAAGATTTGCCCTAGATGTC 2161
GTAGAGACACTTCACCTCCCTTACCTTTTAAAGTTTCTGTTTCTAAACGGGATCTACAG

2102
H L C E V E G M E K F K O K D F A L D V -
AGTGCCAACCCAGCTGTCTCGTGCTGTGAAATGCTCCGAGCAGATGCCAACAAGAAT 2221
TCACGGTTGGTGGACAGGACCAACGACACTTCTACGAGGCTCGTCTACGGTTGTCTTA

b
S A N Q P V L V A V K M L R A D A N K N -
GCCAGGAATGATTTTCTTAAGGAGATAAAGATCATGTCTCGGCTCAAGGACCCAAACATC 2281
CGGTCTTACTAAAAGAATTCTCTATTCTAGTACAGAGCCGAGTTCTGGGTTTGTAG

2222
A R N O F L K E I K I M S R L K D P N I -
ATCCATCTATTAGCTGTGTATCACTGATGACCTCTCTGTATGATCACTGAATACATG 2341
TAGGTAGATAATCGACACACATAGTGACTACTGGGAGAGACATACTAGTGACTTATGTAC

b
I H L L A V C I T D D P L C H I T E Y H -
GAGAATGGAGATCTCAATCAGTTCTTTCCCGCCACGAGCCCCcTAATTCTTCTCCACGC 2401
CTCTTACCTCTAGAGTTAGTCAAAGAAAGGGCGGTGCTCGGGGATTAAAGAAGGAGGTGC

2342
E N G O L N Q F L S R H E P P N S S S S -
GATGTACGCACTGTCAAGTACACCAATCTGAAGTTTATGGCTACCCAAATTGCTCTGGC 2461
CTACATGCGTGACAGTCAATGTGGTTAGACTTCAAATACCGATGGGTTTAAACGAGACCG

2402
D V R T V S Y T N L K F M A T Q I A S G -
ATGAAGTACCTTTCTCTCTTAATTTTGTTCACCGAGATCTGGCCACACGAAACTGTTTA 2521
TACTTCATGGAAGAGAGAGAATTAACATGTGGCTCTAGACCGGTGTGCTTTTGACAAAT

b
M K Y L S S L N F V H R O L A T R N C L -
GTGGGTAAGAACTACACAATCAAGATAGCTGACTTTGGAATGAGCAGGAACCTGTACAGT 2581
CACCCATTCTTGATGTGTAGTTCTATCGACTGAAACCTTACTCGTCTTGGACATGTCA

2522
V G K N Y T I K I A D F G H S R N L Y S -

FIGURE 3D

GGTGACTATTACCGGATCCAGGGCCGGGCAGTGCTCCCTATCCGCTGGATGCTTTGGGAG
 2582 ----- 2641
 CCACTGATAATGGCCTAGGTCCCGGCCCGTCACGAGGGATAGGCGACCTACAGAAACCTC
 b G D Y Y R I Q G R A V L P I R W H S H E -
 AGTATCTTGCTGGGCAAGTTCACCTACAGCAAGTGATGTGGGCCCTTTGGGGTTACTTTG
 2642 ----- 2701
 TCATAGAACGACCCGTTCAAGTGATGTCGTTCACTACACACCCGGAAACCCCAATGAAC
 b S I L L G K F T T A S D V H A F G V T L -
 TGGGAGACTTTCACCTTTTGTCAAGAACAGCCCTATTCACAGCTGTCAGATGAACAGGT
 2702 ----- 2761
 ACCCTCTGAAAGTGGAAACAGTTCTTGTCCGGGATAAGGGTCGACAGTCTACTTGTCCAA
 b M E T F T F C Q E Q P Y S Q L S D E Q V -
 ATTGAGAATACTGGAGAGTTCTTCCGAGACCAAGGGAGGCAGACTTACCTCCCTCAACCA
 2762 ----- 2821
 TAACTCTTATGACCTCTCAAGAAAGGCTCTGGTTCCTCCGCTGAATGGAGGGAGTTGGT
 b I E K T G E F F R D Q G R Q T Y L P Q P -
 GCCATTTGTCTGACTCTGTGTATAAGCTGATGCTCAGCTGCTGGAGAAGAGATACGAAG
 2822 ----- 2881
 CGGTAACAGGACTGAGACACATATTCGACTACGAGTGCAGACCTCTTCTATGCTTC
 b A I C P D S V Y K L H L S C W R R O T K -
 AACCGTCCCTCATTCCAAGAAATCCAACCTTCTGCTCCTTCAACAAGGCGACGAGTGATGC
 2882 ----- 2941
 TTGGCAGGGAGTAAGGTCTTTAGGTGGAAGACGAGGAAGTTGTTCCGCTGCTCACTACG
 b K R P S F Q E I H L L L L Q Q G D E -
 TGTCAGTGCTGGCCATGTTCTACGGCTCAGGTCTCCCTACAAGACCTAOCACCTCACC
 2942 ----- 3001
 ACAGTCACGGACCGGTACAAGGATGCCGAGTCCAGGAGGGATGTTCTGGATGGTGAGTGG
 b
 CATGCCATATGCCACTCCATCTGGACATTTAATGAAACTGAGAGACAGAGGCTTGTGCT
 3002 ----- 3061
 GTACGGATACGGTGAGGTAGACCTGTAAATTACTTTGACTCTCTGTCTCCGAACAAACGA
 b
 TTGCCCTCTTTTCTGCTCACCCCACTCCCTACCCCTGACTCATATATACTTTTTTTT
 3062 ----- 3121
 AACGGGAGAAAAGGACCACTGGGGTGAGGGATGGGGACTGAGTATATATGAAAAA
 b
 TTACATTAAAGAACTAAAAAAAAAAAAAAAAAGGCG
 3122 ----- 3158
 AATGTAATTTCTTGATTTTTTTTTTTTTTTCCGC
 b

CC-440-65-1-2-3-4-5-6-7-8-9-10-11-12-13-14-15-16-17-18-19-20-21-22-23-24-25-26-27-28-29-30-31-32-33-34-35-36-37-38-39-40-41-42-43-44-45-46-47-48-49-50-51-52-53-54-55-56-57-58-59-60-61-62-63-64-65-66-67-68-69-70-71-72-73-74-75-76-77-78-79-80-81-82-83-84-85-86-87-88-89-90-91-92-93-94-95-96-97-98-99-100-101-102-103-104-105-106-107-108-109-110-111-112-113-114-115-116-117-118-119-120-121-122-123-124-125-126-127-128-129-130-131-132-133-134-135-136-137-138-139-140-141-142-143-144-145-146-147-148-149-150-151-152-153-154-155-156-157-158-159-160-161-162-163-164-165-166-167-168-169-170-171-172-173-174-175-176-177-178-179-180-181-182-183-184-185-186-187-188-189-190-191-192-193-194-195-196-197-198-199-200-201-202-203-204-205-206-207-208-209-210-211-212-213-214-215-216-217-218-219-220-221-222-223-224-225-226-227-228-229-230-231-232-233-234-235-236-237-238-239-240-241-242-243-244-245-246-247-248-249-250-251-252-253-254-255-256-257-258-259-260-261-262-263-264-265-266-267-268-269-270-271-272-273-274-275-276-277-278-279-280-281-282-283-284-285-286-287-288-289-290-291-292-293-294-295-296-297-298-299-300-301-302-303-304-305-306-307-308-309-310-311-312-313-314-315-316-317-318-319-320-321-322-323-324-325-326-327-328-329-330-331-332-333-334-335-336-337-338-339-340-341-342-343-344-345-346-347-348-349-350-351-352-353-354-355-356-357-358-359-360-361-362-363-364-365-366-367-368-369-370-371-372-373-374-375-376-377-378-379-380-381-382-383-384-385-386-387-388-389-390-391-392-393-394-395-396-397-398-399-400-401-402-403-404-405-406-407-408-409-410-411-412-413-414-415-416-417-418-419-420-421-422-423-424-425-426-427-428-429-430-431-432-433-434-435-436-437-438-439-440-441-442-443-444-445-446-447-448-449-450-451-452-453-454-455-456-457-458-459-460-461-462-463-464-465-466-467-468-469-470-471-472-473-474-475-476-477-478-479-480-481-482-483-484-485-486-487-488-489-490-491-492-493-494-495-496-497-498-499-500-501-502-503-504-505-506-507-508-509-510-511-512-513-514-515-516-517-518-519-520-521-522-523-524-525-526-527-528-529-530-531-532-533-534-535-536-537-538-539-540-541-542-543-544-545-546-547-548-549-550-551-552-553-554-555-556-557-558-559-560-561-562-563-564-565-566-567-568-569-570-571-572-573-574-575-576-577-578-579-580-581-582-583-584-585-586-587-588-589-590-591-592-593-594-595-596-597-598-599-600-601-602-603-604-605-606-607-608-609-610-611-612-613-614-615-616-617-618-619-620-621-622-623-624-625-626-627-628-629-630-631-632-633-634-635-636-637-638-639-640-641-642-643-644-645-646-647-648-649-650-651-652-653-654-655-656-657-658-659-660-661-662-663-664-665-666-667-668-669-670-671-672-673-674-675-676-677-678-679-680-681-682-683-684-685-686-687-688-689-690-691-692-693-694-695-696-697-698-699-700-701-702-703-704-705-706-707-708-709-710-711-712-713-714-715-716-717-718-719-720-721-722-723-724-725-726-727-728-729-730-731-732-733-734-735-736-737-738-739-740-741-742-743-744-745-746-747-748-749-750-751-752-753-754-755-756-757-758-759-760-761-762-763-764-765-766-767-768-769-770-771-772-773-774-775-776-777-778-779-780-781-782-783-784-785-786-787-788-789-790-791-792-793-794-795-796-797-798-799-800-801-802-803-804-805-806-807-808-809-810-811-812-813-814-815-816-817-818-819-820-821-822-823-824-825-826-827-828-829-830-831-832-833-834-835-836-837-838-839-840-841-842-843-844-845-846-847-848-849-850-851-852-853-854-855-856-857-858-859-860-861-862-863-864-865-866-867-868-869-870-871-872-873-874-875-876-877-878-879-880-881-882-883-884-885-886-887-888-889-890-891-892-893-894-895-896-897-898-899-900-901-902-903-904-905-906-907-908-909-910-911-912-913-914-915-916-917-918-919-920-921-922-923-924-925-926-927-928-929-930-931-932-933-934-935-936-937-938-939-940-941-942-943-944-945-946-947-948-949-950-951-952-953-954-955-956-957-958-959-960-961-962-963-964-965-966-967-968-969-970-971-972-973-974-975-976-977-978-979-980-981-982-983-984-985-986-987-988-989-990-991-992-993-994-995-996-997-998-999-1000-1001-1002-1003-1004-1005-1006-1007-1008-1009-1010-1011-1012-1013-1014-1015-1016-1017-1018-1019-1020-1021-1022-1023-1024-1025-1026-1027-1028-1029-1030-1031-1032-1033-1034-1035-1036-1037-1038-1039-1040-1041-1042-1043-1044-1045-1046-1047-1048-1049-1050-1051-1052-1053-1054-1055-1056-1057-1058-1059-1060-1061-1062-1063-1064-1065-1066-1067-1068-1069-1070-1071-1072-1073-1074-1075-1076-1077-1078-1079-1080-1081-1082-1083-1084-1085-1086-1087-1088-1089-1090-1091-1092-1093-1094-1095-1096-1097-1098-1099-1100-1101-1102-1103-1104-1105-1106-1107-1108-1109-1110-1111-1112-1113-1114-1115-1116-1117-1118-1119-1120-1121-1122-1123-1124-1125-1126-1127-1128-1129-1130-1131-1132-1133-1134-1135-1136-1137-1138-1139-1140-1141-1142-1143-1144-1145-1146-1147-1148-1149-1150-1151-1152-1153-1154-1155-1156-1157-1158-1159-1160-1161-1162-1163-1164-1165-1166-1167-1168-1169-1170-1171-1172-1173-1174-1175-1176-1177-1178-1179-1180-1181-1182-1183-1184-1185-1186-1187-1188-1189-1190-1191-1192-1193-1194-1195-1196-1197-1198-1199-1200-1201-1202-1203-1204-1205-1206-1207-1208-1209-1210-1211-1212-1213-1214-1215-1216-1217-1218-1219-12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FIGURE 4A

1 MILIPRMLLVFLLLPILSSA...KAQVNPATCRYPLGMSGGQIPDEDIT 47 CCK-2
 1 ..MGPEALSSLLLLLVASGDADMKGHFDPACRYALGMQORTIPDSOIS 48 MCK-10
 48 ASSQHSSTAACYGRLDSEEGOGAHCPEIPVEPDOLKEFLQIDLHLFI 97
 49 ASSSHSOSTAARHSRLSSDGOAGCPAGSVFPKE.EEYLQVQLRLHLV 97
 98 TLVGTQGRRAGGHGIEFAPHYKINYSRDGTRWISWRNRHGKQVLDGHSNP 147
 98 ALVGTQGRHAGGLGKEFSRSYRLRYSRDGRRWNGKDRWGQEVISGHEDP 147
 148 YDIFLKDLPPPIVARFVRFPVTDHSHNVCHRVLYGCVWLOGLVSYNAP 197
 148 EGVVLKDLGPPMVARLVRFYPRADRVMSVCLRVLYGCLMRDGLLSYAP 197
 198 AGQQFVLPGGSIITLNDOSVYDG.AVGYSMTGLGQLTDGVSGLDFTQTH 246
 198 VGQTHYLSEA..VYLNOSTYDGHTVGGLOYGGLGQLADGVVGLDDFRKSQ 245
 247 EYHVMPGDYVVGWRNESATRGYIEIMFEFDRIRNFTTKVHCNNHFAKGV 296
 246 ELRVMPGYDYVVGWSNHSFSSGYVEHEFEFORLRAFQAHQVHCNNHHTLGA 295
 297 KIFKEVQC.YFRSEASEWVPNAISFPLVLDVNP SARFVTVPLHHRKASA 345
 296 RLPGGVECRFRRGPAMAWEGEPMRHNHGGNLGDPRAVSVPLGGRVARF 345
 346 IKQYHFADTMHFESEITFQSOAHYNNSEALPTS..... 380
 346 LQCRFLFAGPMLLFSEISFISO.VVNNSSPALGGTFPPAPMPPGPPPTN 394
 381PHAPTYYDPMKVDOSNTRILIGCLVAIIFILLAIIVILNRQFWQ 426
 395 FSSLELEPRGQQPVAKAEGSPTAILIGCLVAIILLILLI IALMLKRLKWR 444
 427 KMLEKASRRMLDOENTVSLSLPSDSSMFNNHRSSSPSEQGSHSTYDRIFP 476
 445 RLLSKAERRVLEELTVHLSVPGOTILINRPPGPREP..... 481
 477 LRPOYQEPSRLIRKLPEFAPGEEESGCSG.....VVKPVQPSGPEGV 518
 482 ..PPYQEP RPGRNPPHSAPCVNGSAYSQDYHEPEKPGAPLPPPPQHSV 521
 519 PHYAEADIVR...VTGGNTYVPAVTHDLLSGKDVAVEEFPRKLLTFKEK 562
 530 PHYAEADIVTLGGVTGGNTYAVPALPPGAVDGPVRV.OFPRSRLRFKEK 578
 569 LGEGQFGEVHLCEVEGMEKFKDKDFALDVSANQPVLVAVKMLRADANKNA 618
 579 LGEGQFGEVHLCEVOSPQOLVSLDFPLNVRKGHPLLVAVKILRPDANKNA 628
 619 RNDFLKEIKHSRLKDPNIHLLAVCITODPLCHITEYHENGDLNQFLSR 668
 629 RNDFLKEVKHSRLKDPNIIRLLGVCVQDOPLCNITDYHENGDLNQFLSA 678
 669 HE.....PPNSSSDVRTVSYTHLKFMATQIASGHKYLSSLNFVHR 709
 679 HQLEDKAAEGAPGQQAAGPTISYPMLLVAAQIASGNYRLATLNFVHR 728
 710 DLATRNCLVGKNTYIKIADFQMSRNLYSGDYRIQGRAVLPIRMMSVESI 759
 729 DLATRNCLVGENFTIKIADFQMSRNLYAGDYRVQGRAVLPIRMMAHECI 778
 760 LLGKFTTASDVHAFGVTLWETFTFCQEQPYSQLSDEQVIENAGEFFRDQ 809
 779 LHGKFTTASDVHAFGVTLWEVLMLCRAQPFQQLTDEQVIENAGEFFRDQ 828
 810 RQTYLPQPAICPDSVYKHLHLSCHRDTKNRPSFQEIHLILLQQGE.. 855
 829 RQVYLSRPPACPGGLYELMLRCVRSRESEQRPPESQLHRLAEDALNTV 876

Transmembrane region

ATP-
binding site

00440:00440

Figure 4B

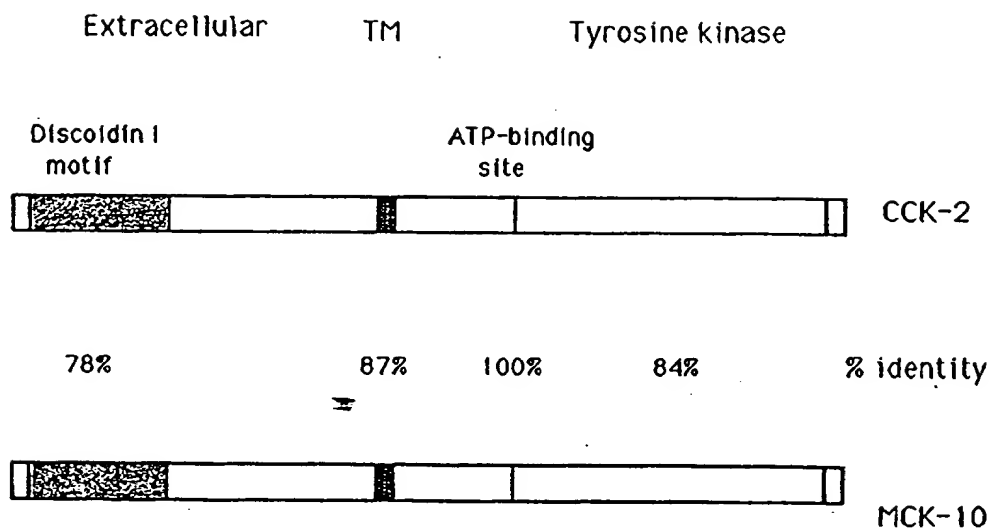


FIGURE 5A

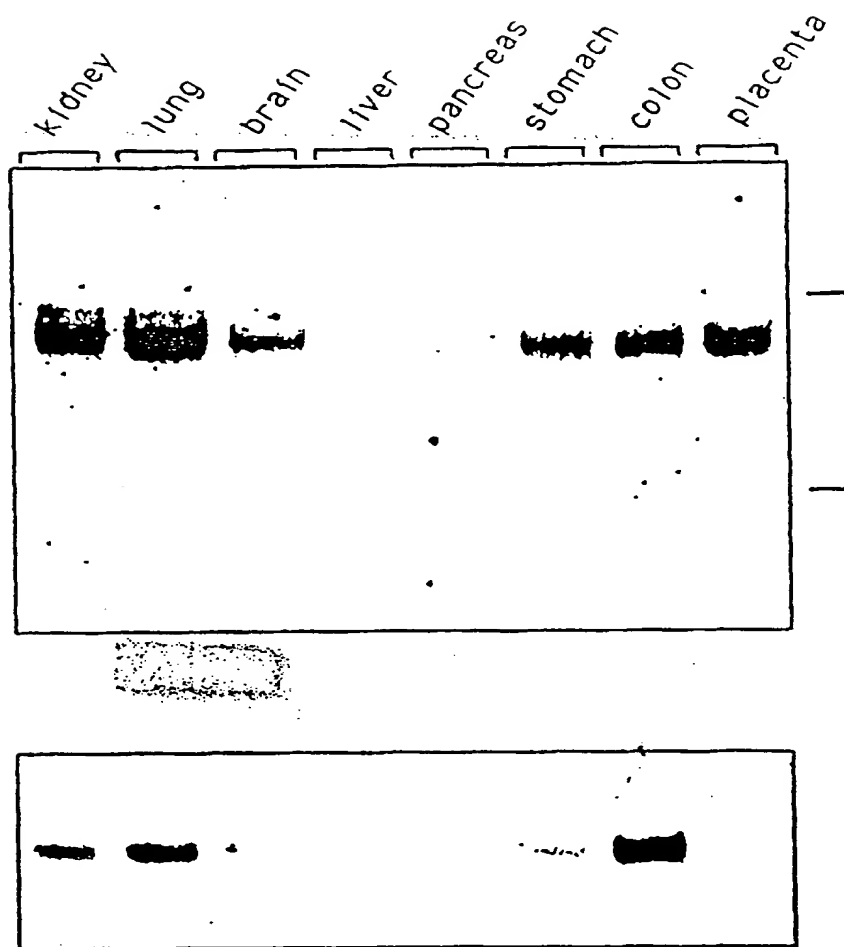


FIGURE 5B

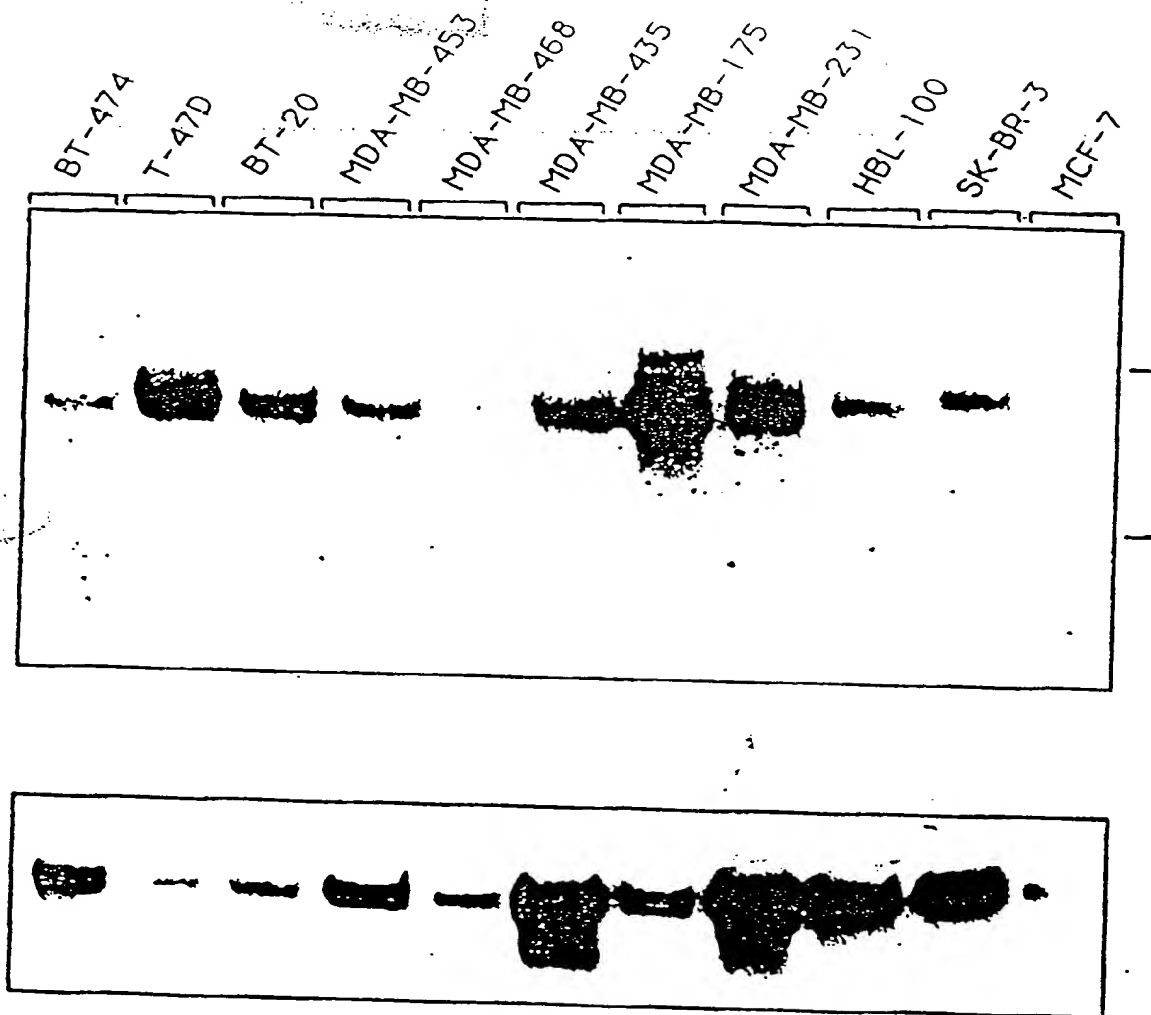


FIGURE 5C

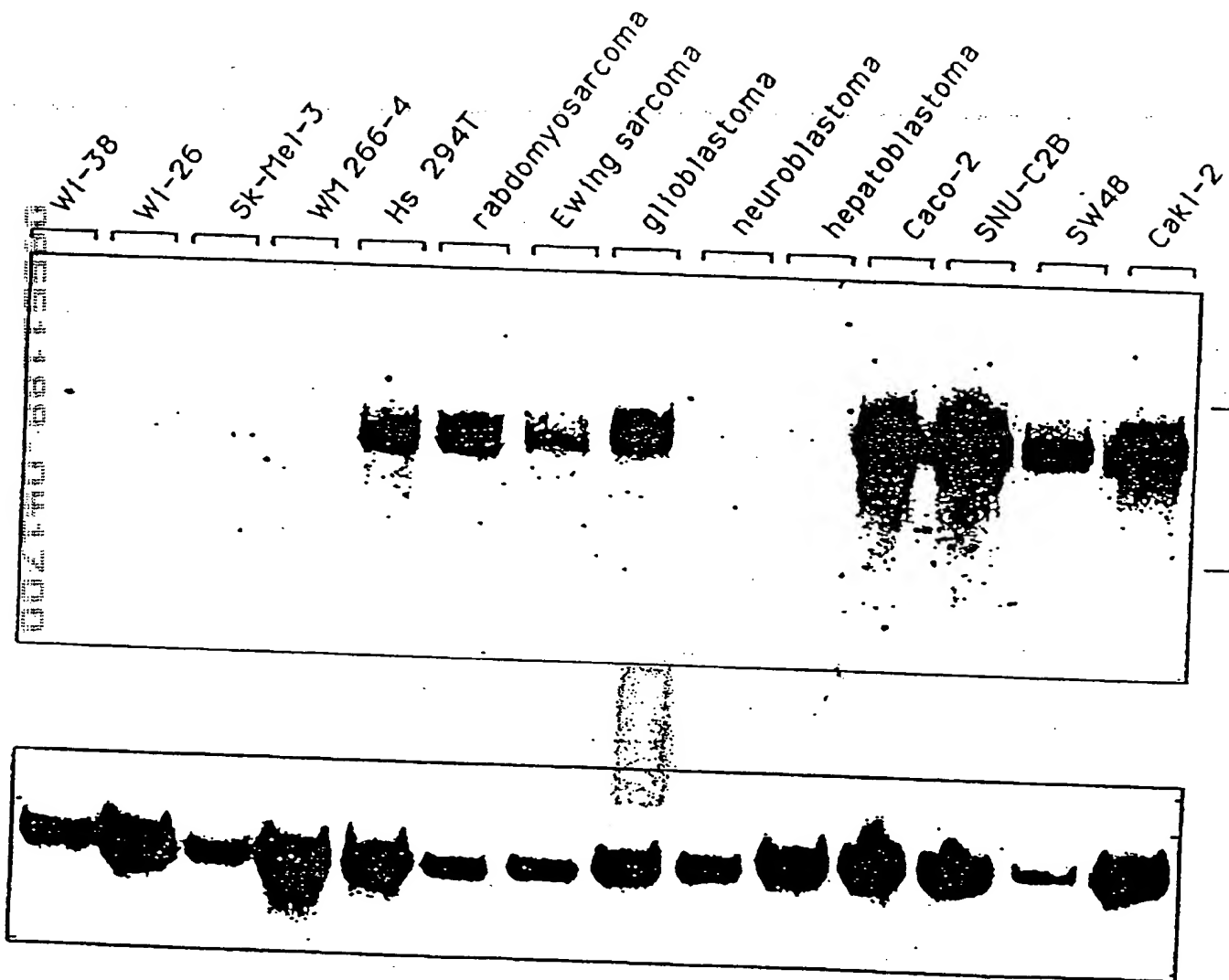


FIGURE 6A

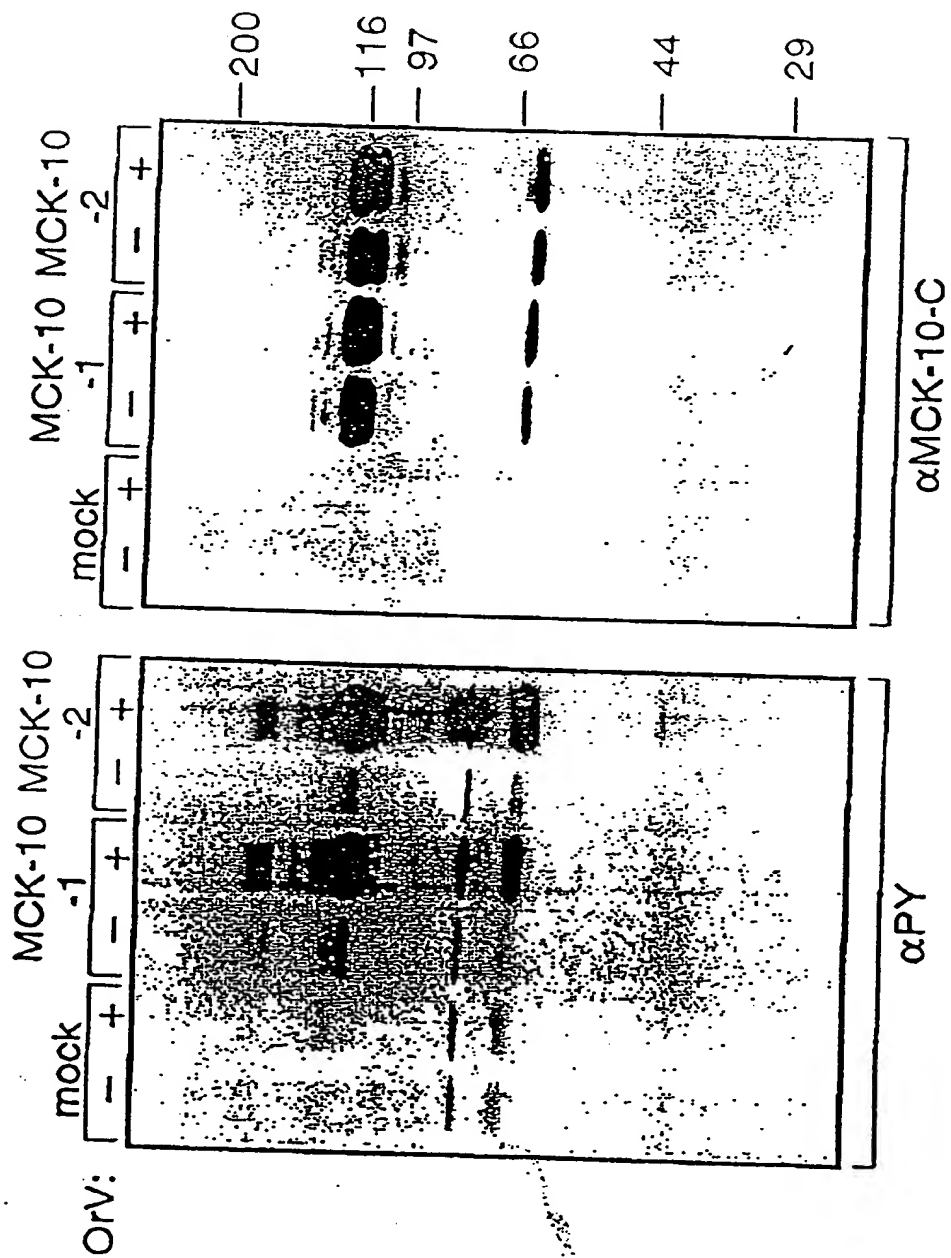


FIGURE 6B

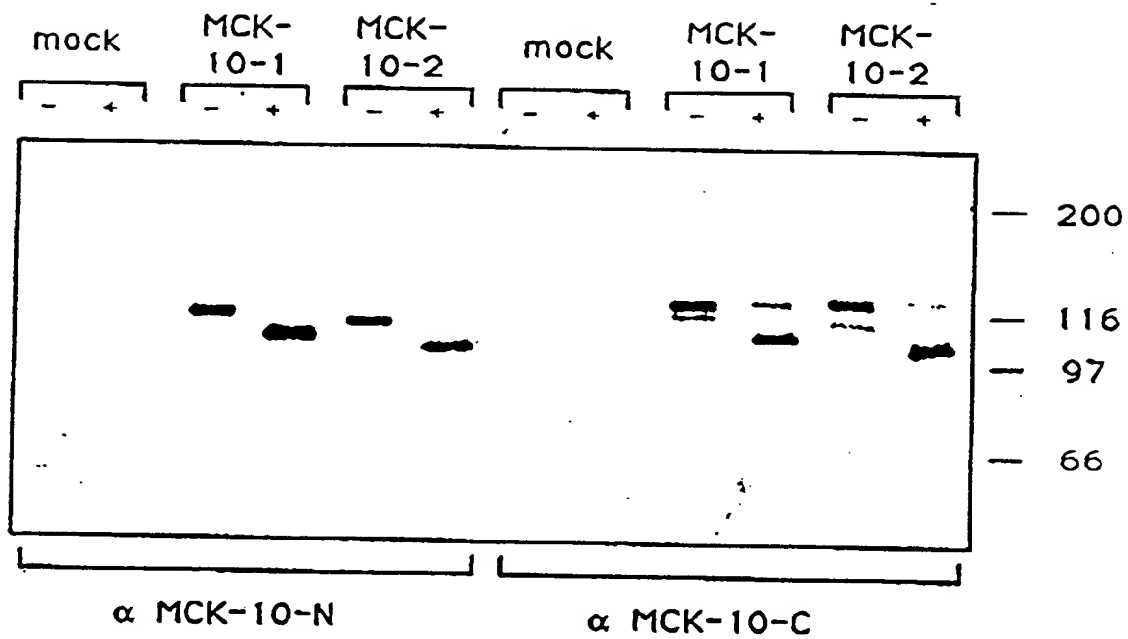
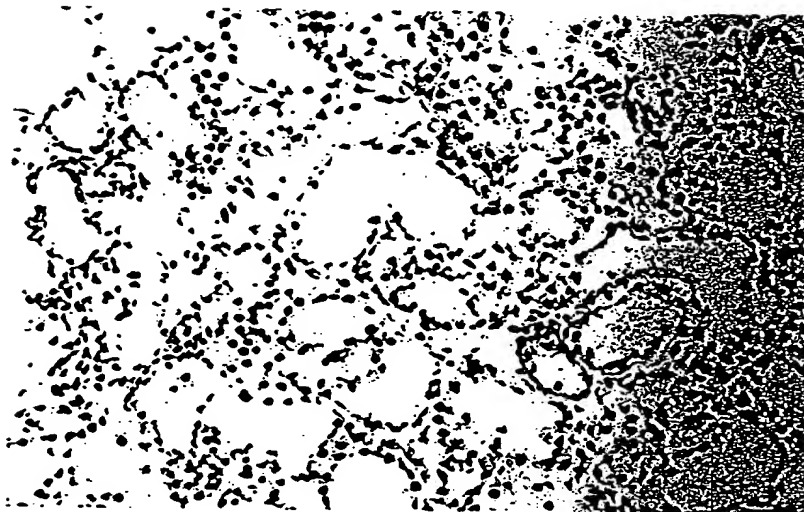


FIGURE 7A

lightfield



darkfield

FIGURE 7B

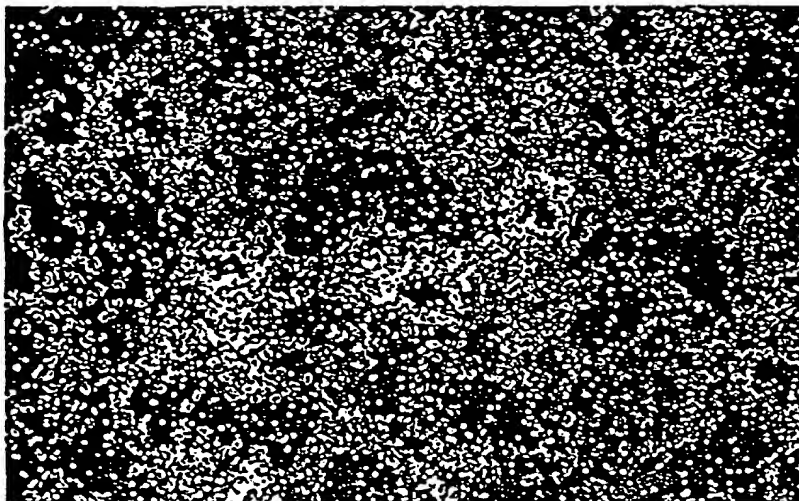
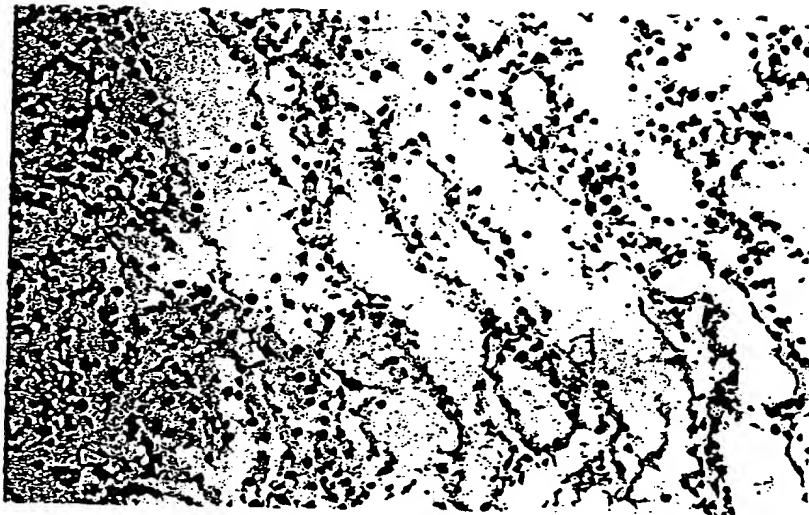


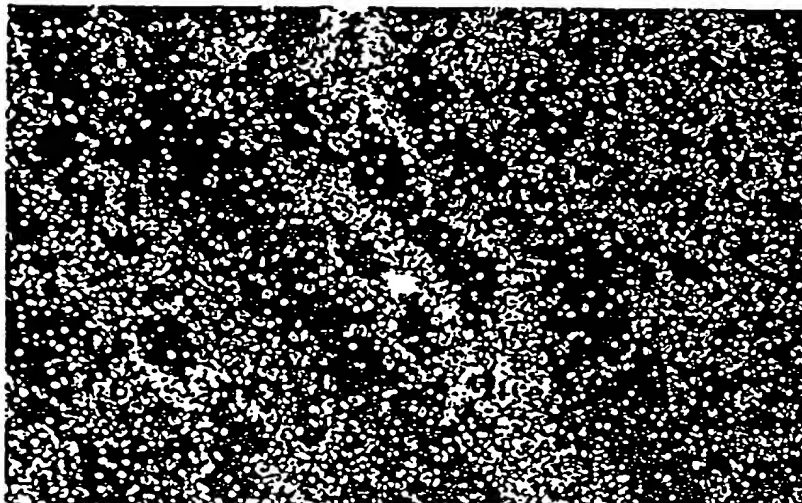
FIGURE 8A

lightfield



darkfield

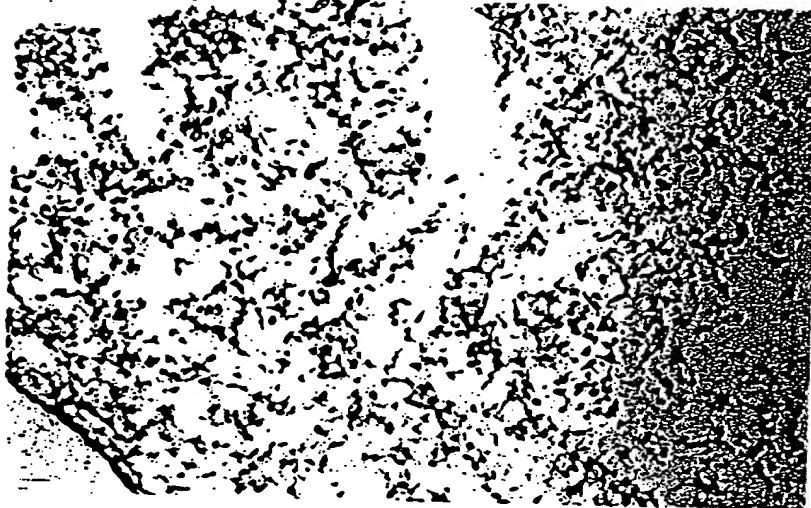
FIGURE 8B



002740 001500

FIGURE 9A

lightfield



darkfield

FIGURE 9B

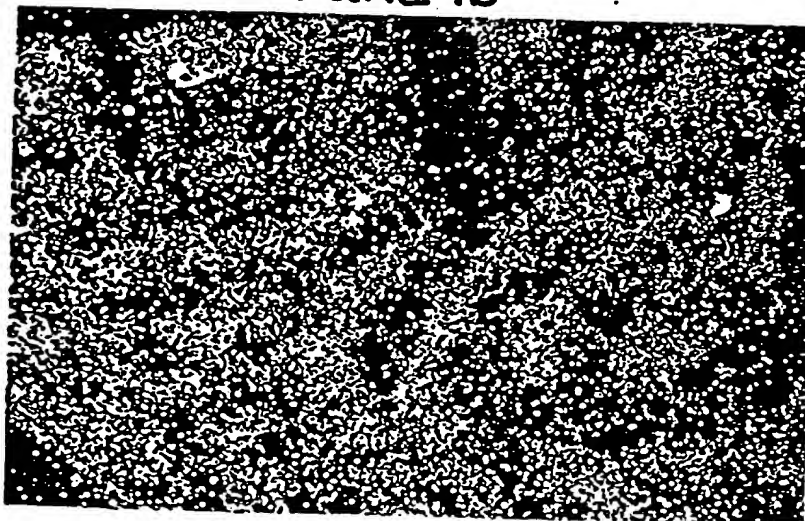
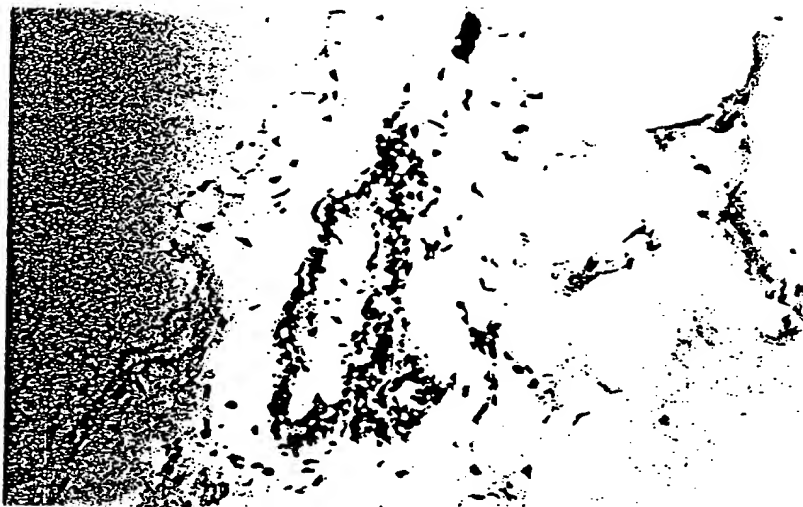


FIGURE 10A

lightfield



darkfield

FIGURE 10B

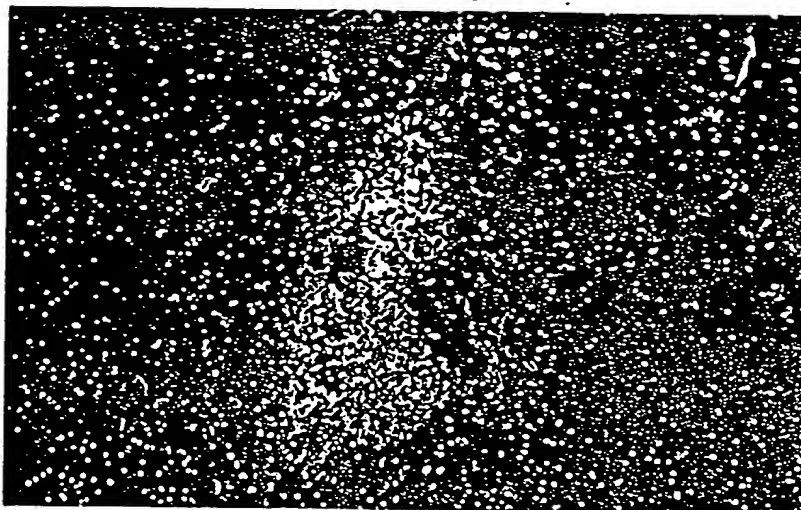
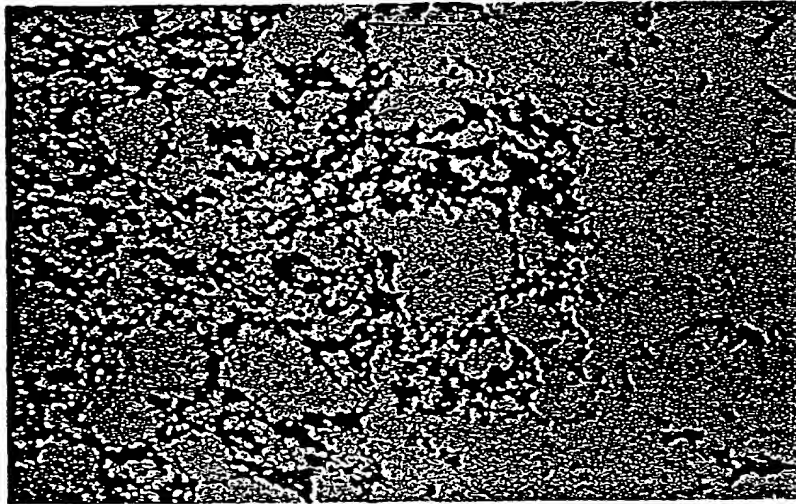


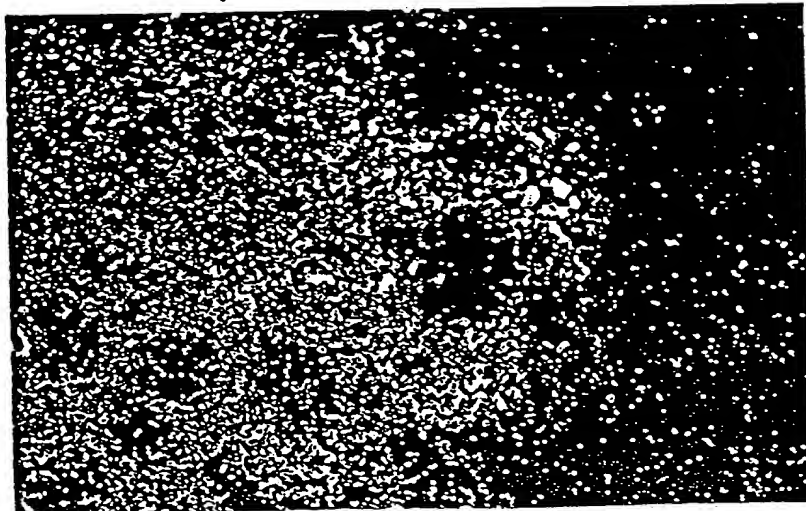
FIGURE IIA

lightfield

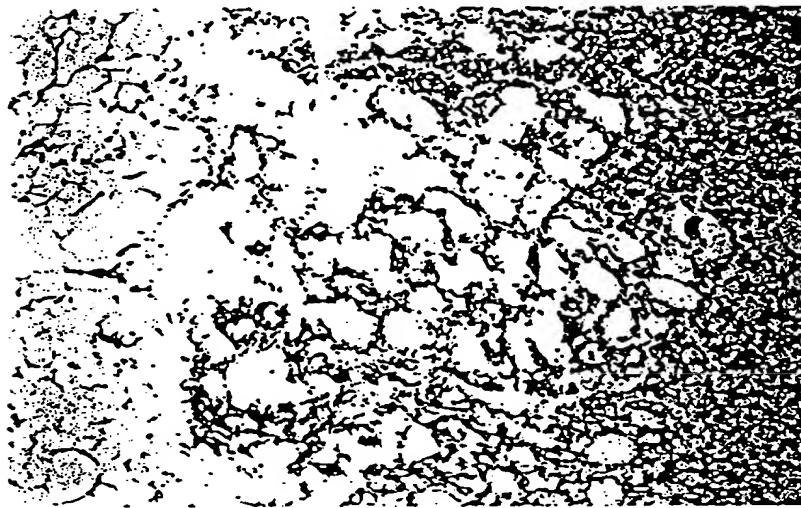


darkfield

FIGURE IIB



lightfield



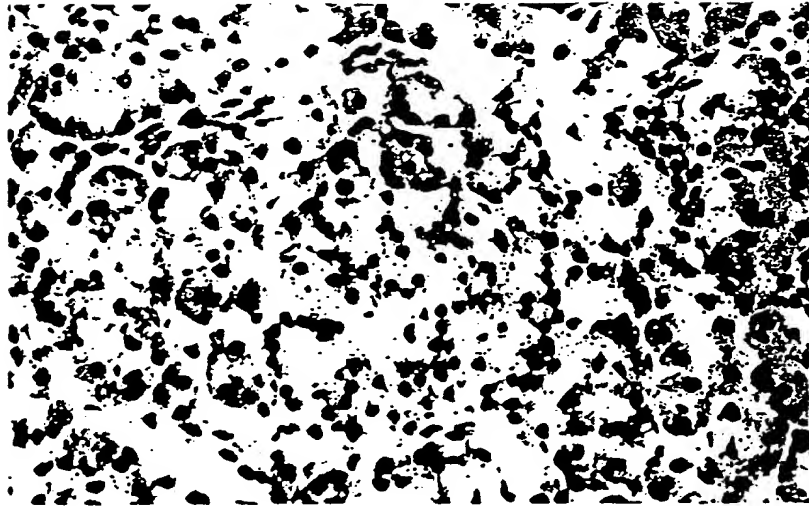
darkfield

FIGURE 12B



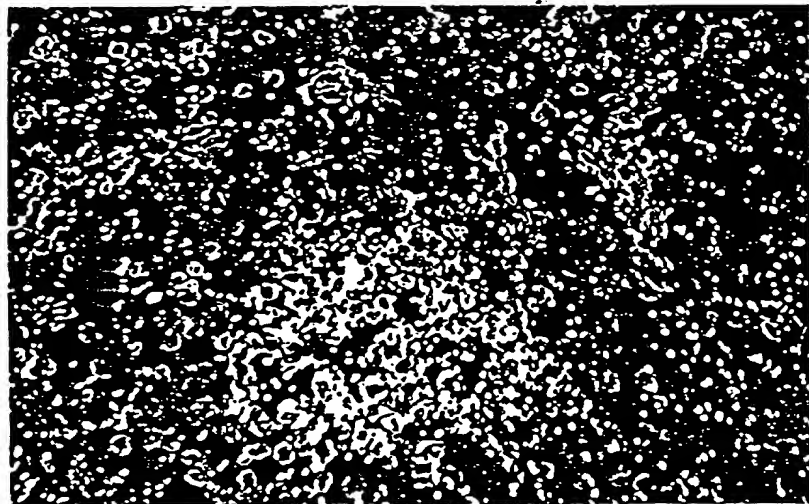
FIGURE 13A

lightfield



darkfield

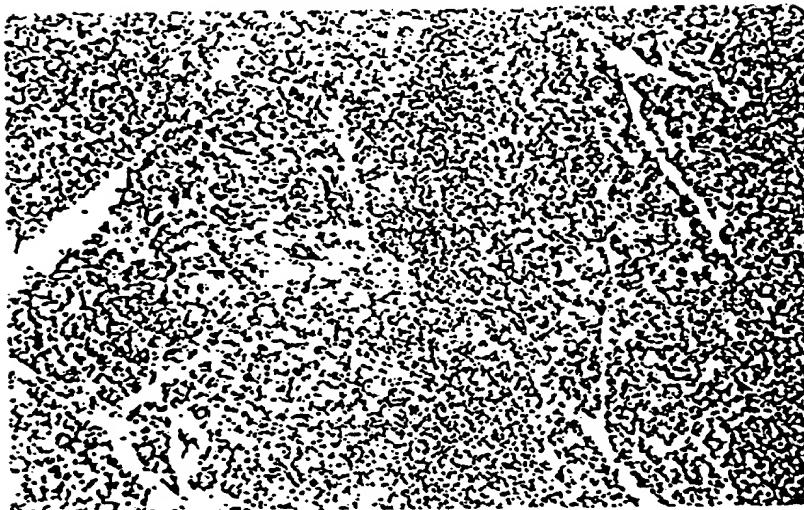
FIGURE 13B



002470-00113500

FIGURE 14A

lightfield



darkfield

FIGURE 14B



002740 851560

FIGURE 15A

lightfield



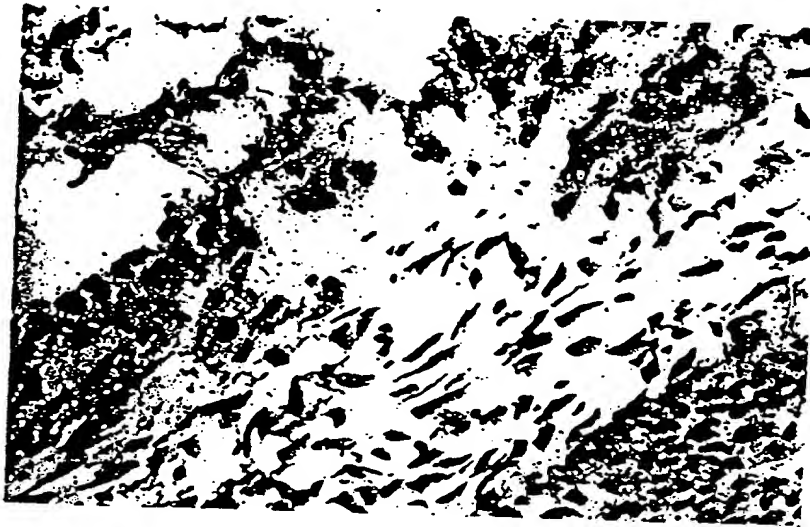
darkfield

FIGURE 15B



FIGURE 16A

lightfield



darkfield

FIGURE 16B



FIGURE 17A

lightfield



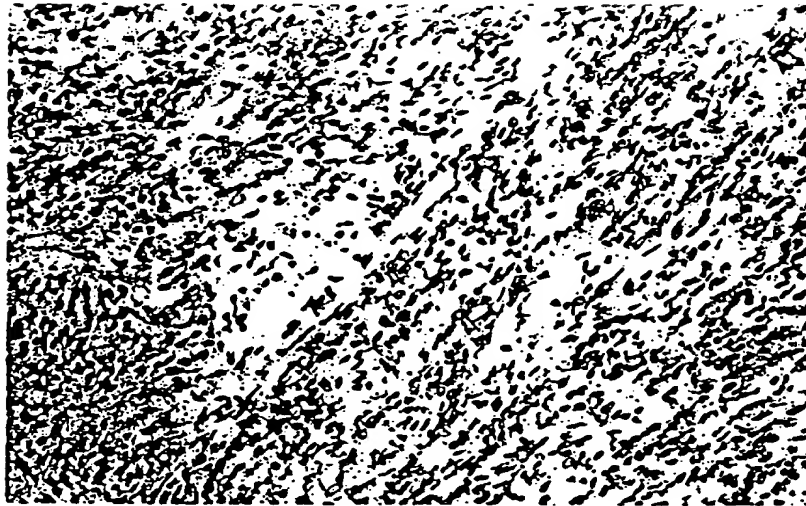
darkfield

FIGURE 17B



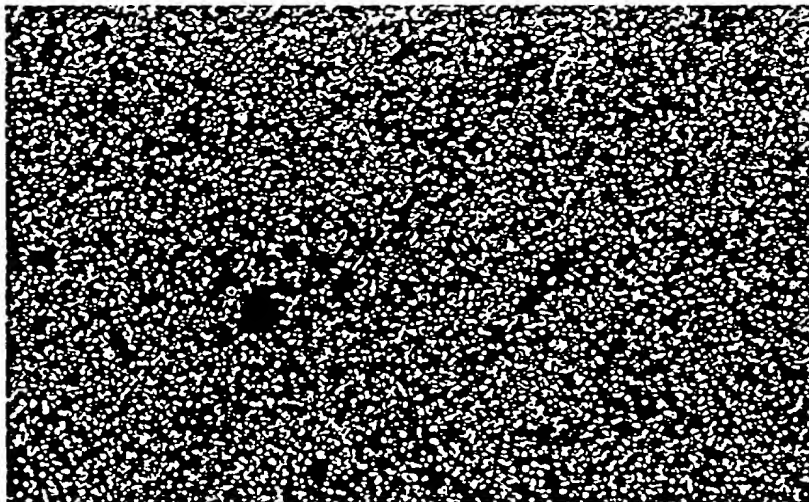
FIGURE 18A

lightfield



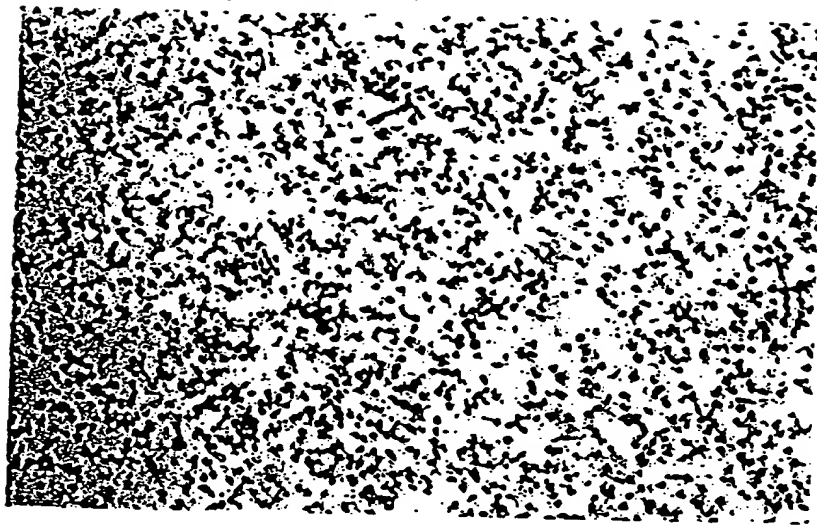
darkfield

FIGURE 18B



00440 004500

lightfield



darkfield

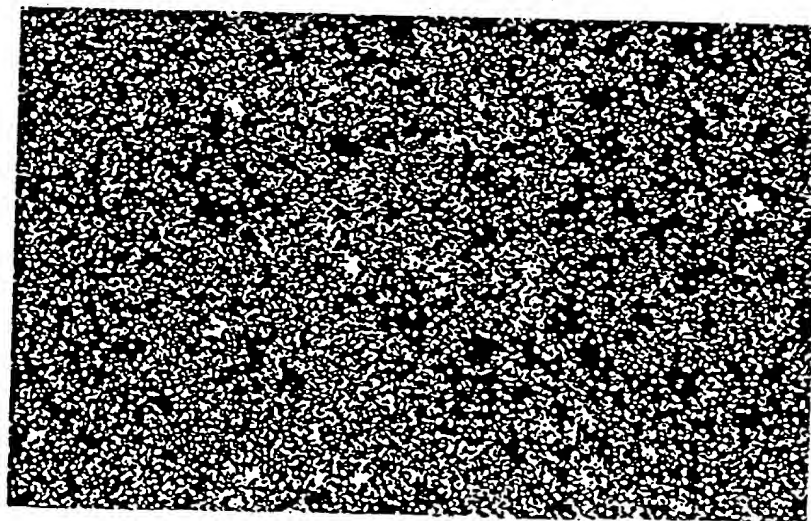
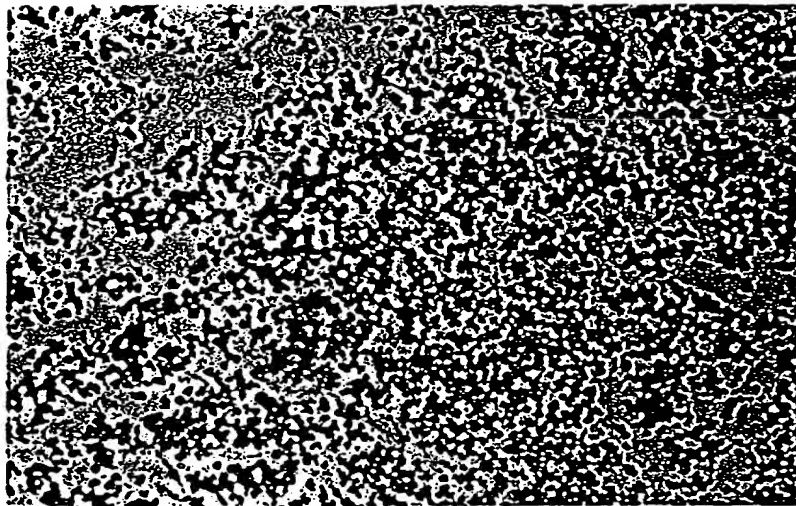


FIGURE 20A

lightfield



darkfield

FIGURE 20B:

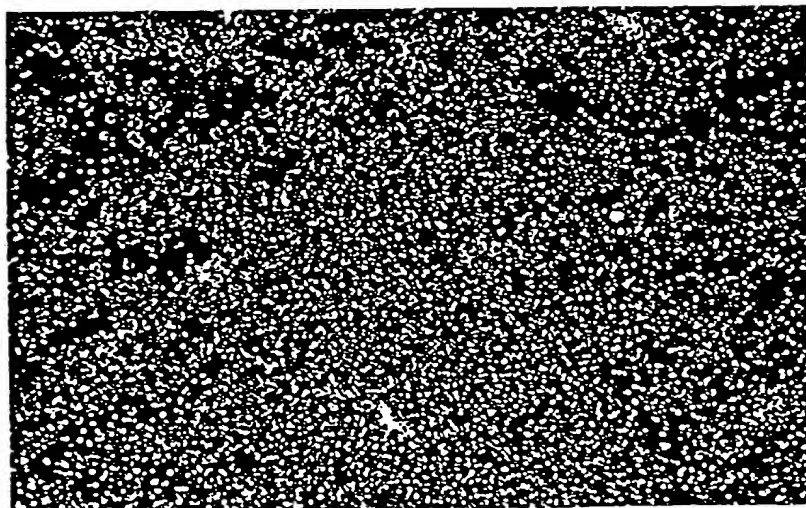
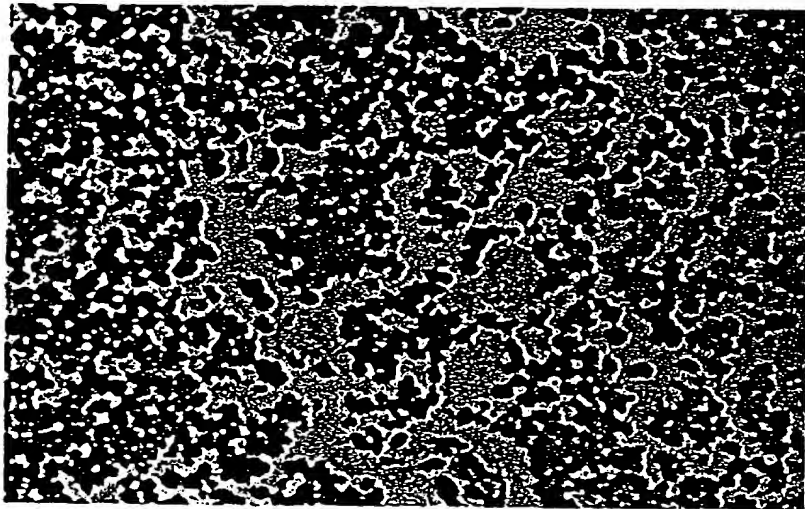


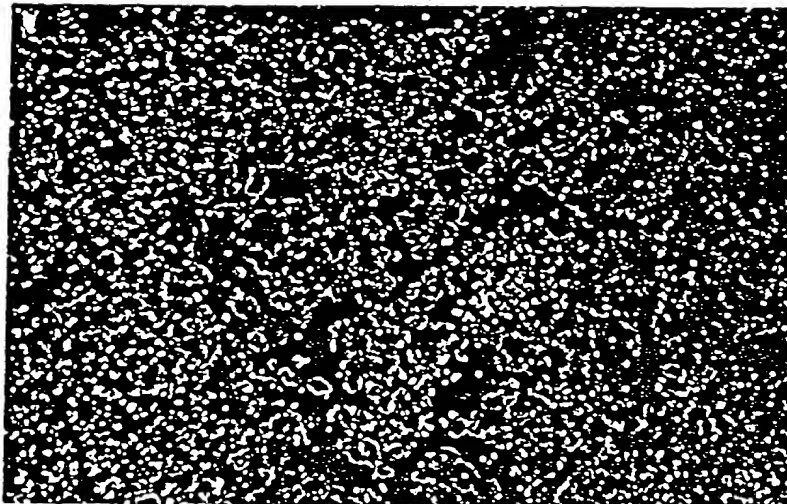
FIGURE 21A

lightfield



darkfield

FIGURE 21B



002140 00114460